

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: February 10, 2006, 05:26:42 / Search time 4815 Seconds
(without alignments)
10270.779 Million cell updates/sec

Title: US-10-600-997-7

Perfect score: 870
Sequence: 1 atgagagacatgcctgcacat.....ccatcgtcgcagaggttaa 870

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:
1: gb Da:
2: gb In:
3: gb Env:
4: gb Om:
5: gb Ov:
6: gb Pac:
7: gb Ph:
8: gb Pr:
9: gb Ro:
10: gb Sts:
11: gb Sy:
12: gb Un:
13: gb Vt:
14: gb Htg:
15: gb Pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	870	8 AY293286	AY293286 Homo sapi
2	857.2	98.5	870	6 CQ947366	CQ947366 Sequence
3	857.2	98.5	990	6 CQ947428	CQ947428 Sequence
4	854	98.2	1066	6 C8105855	C8105855 Sequence
5	846	97.2	3002	8 AK131204	AK131204 Homo sapi
6	764.2	87.8	777	6 CQ947365	CQ947365 Sequence
7	704.2	80.9	717	6 CQ947364	CQ947364 Sequence
8	527.6	60.6	534	6 CQ947360	CQ947360 Sequence
9	520.2	59.8	726	6 BD060983	BD060983 Sequence
10	466.2	53.6	444	6 CQ947358	CQ947358 Sequence
11	437.6	50.3	444	6 CQ947359	CQ947359 Sequence
12	425	48.9	769	6 C8035517	C8035517 Sequence
13	425	48.9	769	6 C8044469	C8044469 Sequence
14	402.8	46.3	1903	6 BD131124	BD131124 45 human
15	402.8	46.3	1903	6 C8132603	C8132603 Sequence
16	388	44.6	1903	6 AR339778	AR339778 Sequence
17	378	43.4	1940	6 CQ947363	CQ947363 Sequence
18	378	43.4	1940	6 BD131144	BD131144 45 human

19	378	43.4	1940	6 C8132623	C8132623 Sequence
20	378	43.4	1940	6 AR339797	AR339797 Sequence
21	376.2	43.2	381	6 CQ947357	CQ947357 Sequence
22	326.6	37.5	333	6 CQ947362	CQ947362 Sequence
23	315.8	36.3	127852	8 AC092894	AC092894 Homo sapi
24	315.8	36.3	143094	14 AC024131	AC024131 Homo sapi
25	315.8	36.3	175135	14 AC079211	AC079211 Homo sapi
26	285.2	32.8	2230	9 BC092588	BC092588 Rattus no
27	276.6	31.8	422	6 AX779565	AX779565 Sequence
28	276.6	31.8	465	6 AX780935	AX780935 Sequence
29	275.6	31.7	921	9 AY293285	AY293285 Mus muscu
30	267.6	30.8	921	6 CQ947408	CQ947408 Sequence
31	267.6	30.8	1250	6 CQ947429	CQ947429 Sequence
32	267.6	30.8	1276	6 CQ947433	CQ947433 Sequence
33	264.6	30.4	957	6 CQ947430	CQ947430 Sequence
34	264.6	30.4	1722	6 CQ947431	CQ947431 Sequence
35	258.8	29.7	927	9 AY590499	AY590499 Rattus no
36	254.2	29.2	831	6 CQ947407	CQ947407 Sequence
37	236.8	27.2	750	6 CQ947406	CQ947406 Sequence
38	233	26.8	319	6 BD026702	BD026702 Sequence
39	233	26.8	319	6 AX887092	AX887092 Sequence
40	199.4	22.9	201	6 CQ947348	CQ947348 Sequence
41	198.4	22.8	201	6 CQ947361	CQ947361 Sequence
42	157.2	18.1	537	6 CQ947413	CQ947413 Sequence
43	157.2	18.1	537	6 CQ947437	CQ947437 Sequence
44	156.4	18.0	378	6 CQ947405	CQ947405 Sequence
45	149.2	17.1	340	6 CQ947400	CQ947400 Sequence

ALIGNMENTS

RESULT 1
AY293286
LOCUS
DEFINITION
Homo sapiens B and T lymphocyte attenuator (BTIA) mRNA, complete cds.
ACCESSION
AY293286
VERSION
AY293286.1
KEYWORDS
GI:31860026
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 870)
Watanabe, N., Gavriel, M., Sedy, J.R., Yang, J., Fallarino, F., Loftin, S.K., Hurchla, M.A., Zimmerman, N., Sim, J., Zang, X., Murphy, T.L., Russell, J.H., Allison, J.P. and Murphy, K.W.
BTIA is a lymphocyte inhibitory receptor with similarities to CTLA-4 and PD-1
Nat. Immunol. (2003) In press
JOURNAL
2 (bases 1 to 870)
Murphy, K.W., Watanabe, N., Yang, J. and Murphy, T.L.
Direct Submission (08-MAY-2003) Pathology, Washington University, 660 S. Euclid, St. Louis, MO 63110, USA
TITLES
JOURNAL
BTIA-4 and PD-1
AUTHORS
JOURNAL
BTIA-4 and PD-1
REFERENCES
JOURNAL
BTIA-4 and PD-1
AUTHORS
JOURNAL
BTIA-4 and PD-1
FEATURES
source
1. 870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="Ramos"
1. 870
/gene="BTIA"
1. 870
/note="Immunoregulatory inhibitory receptor; similar to CTLA-4 and PD-1"
/product="B and T lymphocyte attenuator"
/protein_id="AA044003.1"
/db_xref="GI:31860027"

(3)

Db 337 AACCTGAAGATAGCAAAACAAAGTGAAGAGAAAGAAACATTTCATTTTCATTTCTA 396
 Qy 301 CATTGGAACCAATGCTCTTAATGACATGAGGTATACCGCTGTTCTGCAAAATTTTCA 360
 Db 397 CATTGGAACCAATGCTCTTAATGACATGAGGTATACCGCTGTTCTGCAAAATTTTCA 456
 Qy 361 TCTAATCTGATGAAGCACTCAACCTTTAATGACAGATGTAAGAGTCCCTCA 420
 Db 457 TCTAATCTGATGAAGCACTCAACCTTTAATGACAGATGTAAGAGTCCCTCA 516
 Qy 421 GAAAGACCTCCAGAGAGAAAGTGAAGCAAGCCCTGCTCTGTAATGTTTACTTCT 480
 Db 517 GAAAGACCTCCAGAGAGAAAGTGAAGCAAGCCCTGCTCTGTAATGTTTACTTCT 576
 Qy 481 TTGGGGGGAATGGCTCTACTGATCACTAGTCTGCTGTTCTGCTGCTGAGAG 540
 Db 577 TTGGGGGGAATGGCTCTACTGATCACTAGTCTGCTGTTCTGCTGCTGAGAG 636
 Qy 541 CACCAAGGAAGCAAAATGAATCTCTGACACAGAGAGAGAAATTAATCTGTTGAT 600
 Db 637 CACCAAGGAAGCAAAATGAATCTCTGACACAGAGAGAGAAATTAATCTGTTGAT 696
 Qy 601 GCTCACTTAAGAGAGCAAAACAGAGACCAAGCAAAATTTCCAGTACTGCTA 660
 Db 697 GCTCACTTAAGAGAGCAAAACAGAGACCAAGCAAAATTTCCAGTACTGCTA 756
 Qy 661 TCAGAACTGGAATTTATGATATGACCTGACCTTTGTTCAAGATGCAAGAGGCT 720
 Db 757 TCAGAACTGGAATTTATGATATGACCTGACCTTTGTTCAAGATGCAAGAGGCT 816
 Qy 721 GAAATTTGTTTAAATTCATGCTGAGAGAAACAAACAGGCAATTTTATGCTTCCCTG 780
 Db 817 GAAATTTGTTTAAATTCATGCTGAGAGAAACAAACAGGCAATTTTATGCTTCCCTG 876
 Qy 781 AACCAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 877 AACCAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 936
 Qy 841 GAATATGATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
 Db 937 GAATATGATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966

RESULT 7

US-10-371-341-1
 / Sequence 1, Application US/10371341
 / Publication No.: US20040091884A1
 / GENERAL INFORMATION:
 / APPLICANT: HILARY CLARK
 / APPLICANT: DANIEL L. EATON
 / APPLICANT: AUSTIN L. GURNEY
 / APPLICANT: BERND WRANIK
 / TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF
 / TITLE OF INVENTION: IMMUNE RELATED DISEASES
 / FILE REFERENCE: P1996R1-US
 / CURRENT APPLICATION NUMBER: US/10/371,341
 / PRIOR FILING DATE: 2003-07-19
 / PRIOR APPLICATION NUMBER: US 60/421,236
 / NUMBER OF SEQ ID NOS: 2
 / SEQ ID NO: 1
 / LENGTH: 1066
 / TYPE: DNA
 / ORGANISM: Homo sapien
 US-10-371-341-1

Query Match 98.2% Score 854, DB 7, Length 1066;
 Best Local Similarity 98.9% Pred No. 2.8e-246;
 Matches 860, Conservative 0, Mismatches 10, Indels 0, Gaps 0;
 1 ATGAAGACATTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 60

Db 24 ATGAAGACATTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 83
 Qy 61 CCATATCTGACATCTGGAACATCCATGAGAGAAATCAATGATGATGATGATGATGAT 120
 Db 84 CCATATCTGACATCTGGAACATCCATGAGAGAAATCAATGATGATGATGATGATGAT 143
 Qy 121 AAGAGCAATCTGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 144 AAGAGCAATCTGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
 Qy 181 AATATCTGCTAACAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 204 AATATCTGCTAACAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 263
 Qy 241 AATCTGAAGATAGCAAAACAAAGTGAAGAGAGAAACATTTCAATTTTCTGATCTA 300
 Db 264 AATCTGAAGATAGCAAAACAAAGTGAAGAGAGAGAAACATTTCAATTTTCTGATCTA 323
 Qy 301 CATTGGAACCAATGCTCTTAATGACATGAGGTATACCGCTGTTCTGCAAAATTTTCA 360
 Db 324 CATTGGAACCAATGCTCTTAATGACATGAGGTATACCGCTGTTCTGCAAAATTTTCA 383
 Qy 361 TCTAATCTGATGAAGCACTCAACCTTTAATGACAGATGTAAGAGTCCCTCA 420
 Db 384 TCTAATCTGATGAAGCACTCAACCTTTAATGACAGATGTAAGAGTCCCTCA 443
 Qy 421 GAAAGACCTCCAGAGAGAAAGTGAAGCAAGCCCTGCTCTGTAATGTTTACTTCT 480
 Db 444 GAAAGACCTCCAGAGAGAAAGTGAAGCAAGCCCTGCTCTGTAATGTTTACTTCT 503
 Qy 481 TTGGGGGGAATGGCTCTACTGATCACTAGTCTGCTGTTCTGCTGCTGAGAG 540
 Db 504 TTGGGGGGAATGGCTCTACTGATCACTAGTCTGCTGTTCTGCTGCTGAGAG 563
 Qy 541 CACCAAGGAAGCAAAATGAATCTCTGACACAGAGAGAGAAATTAATCTGTTGAT 600
 Db 564 CACCAAGGAAGCAAAATGAATCTCTGACACAGAGAGAGAAATTAATCTGTTGAT 623
 Qy 601 GCTCACTTAAGAGAGCAAAACAGAGACCAAGCAAAATTTCCAGTACTGCTA 660
 Db 624 GCTCACTTAAGAGAGCAAAACAGAGACCAAGCAAAATTTCCAGTACTGCTA 683
 Qy 661 TCAGAACTGGAATTTATGATATGACCTGACCTTTGTTCAAGATGCAAGAGGCT 720
 Db 684 TCAGAACTGGAATTTATGATATGACCTGACCTTTGTTCAAGATGCAAGAGGCT 743
 Qy 721 GAAATTTGTTTAAATTCATGCTGAGAGAAACAAACAGGCAATTTTATGCTTCCCTG 780
 Db 744 GAAATTTGTTTAAATTCATGCTGAGAGAAACAAACAGGCAATTTTATGCTTCCCTG 803
 Qy 781 AACCAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 804 AACCAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
 Qy 841 GAATATGATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
 Db 864 GAATATGATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893

RESULT 8

US-10-989-826-27
 / Sequence 27, Application US/10989826
 / Publication No. US20050238650A1
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: Crowley, Craig
 / APPLICANT: De Sauvage, Frederic J.
 / APPLICANT: Eaton, Daniel L.
 / APPLICANT: Ebens, Allen
 / APPLICANT: Polson, Andrew
 / APPLICANT: Smith, Victoria
 / TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of
 / TITLE OF INVENTION: Hematopoietic Origin

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 8, 2006, 16:54:56 / Search time 118.5 Seconds
(without alignments)
1019.010 Million cell updates/sec

Title: US-10-600-997-6
Perfect score: 1552
Sequence: 1 MKTLPAMLTGKGLFWVFPLI.....RLANVKEAPTEVASICRS 289

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA Main:
1: /cgm2_6/ptcdat/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/ptcdat/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgm2_6/ptcdat/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgm2_6/ptcdat/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgm2_6/ptcdat/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgm2_6/ptcdat/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	100.0	289	4	US-10-371-341-2
2	1552	100.0	289	4	US-10-600-997-6
3	1552	100.0	289	5	US-10-831-622-21
4	1552	100.0	289	5	US-10-964-215-21
5	1552	100.0	289	5	US-10-989-826-28
6	1552	100.0	521	5	US-10-831-622-28
7	1552	100.0	521	5	US-10-964-215-98
8	1516	97.7	289	4	US-10-600-997-8
9	1383	89.1	259	5	US-10-831-622-20
10	1383	89.1	259	5	US-10-964-215-20
11	1282	82.6	239	5	US-10-831-622-19
12	1282	82.6	239	5	US-10-964-215-19
13	1256	80.9	241	4	US-10-471-449-10
14	980	63.1	178	5	US-10-831-622-15
15	980	63.1	178	5	US-10-964-215-15
16	860	55.4	157	5	US-10-831-622-13
17	860	55.4	157	5	US-10-964-215-13
18	811	52.3	148	5	US-10-831-622-14
19	811	52.3	148	5	US-10-964-215-14
20	745.5	48.0	212	4	US-10-063-548-88
21	745.5	48.0	212	5	US-10-918-446-88
22	745.5	48.0	212	6	US-11-002-755-88
23	745.5	48.0	212	6	US-11-002-756-88
24	743.5	47.9	306	4	US-10-600-997-5
25	743.5	47.9	306	4	US-10-600-997-10
26	739.5	47.6	306	5	US-10-831-622-63
27	739.5	47.6	306	5	US-10-964-215-63

28	739.5	47.6	538	5	US-10-831-622-99	Sequence 99, Appl
29	739.5	47.6	538	5	US-10-964-215-99	Sequence 99, Appl
30	692	44.6	132	5	US-10-831-622-18	Sequence 18, Appl
31	692	44.6	132	5	US-10-964-215-18	Sequence 18, Appl
32	691	44.5	127	5	US-10-831-622-12	Sequence 12, Appl
33	691	44.5	127	5	US-10-964-215-12	Sequence 12, Appl
34	673.5	43.4	277	5	US-10-831-622-62	Sequence 62, Appl
35	673.5	43.4	277	5	US-10-964-215-62	Sequence 62, Appl
36	635.5	40.9	250	5	US-10-831-622-61	Sequence 61, Appl
37	635.5	40.9	250	5	US-10-964-215-61	Sequence 61, Appl
38	572	36.9	111	5	US-10-831-622-17	Sequence 17, Appl
39	572	36.9	111	5	US-10-964-215-17	Sequence 17, Appl
40	516	33.2	102	4	US-10-062-548-107	Sequence 107, App
41	516	33.2	102	5	US-10-918-446-107	Sequence 107, App
42	516	33.2	102	6	US-11-002-755-107	Sequence 107, App
43	516	33.2	102	6	US-11-002-756-107	Sequence 107, App
44	474	30.5	204	5	US-10-831-622-57	Sequence 57, Appl
45	474	30.5	204	5	US-10-964-215-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-10-371-341-2
Sequence 2, Application US/10371341
Publication No. US20040091884A1
GENERAL INFORMATION:
APPLICANT: HILARY CLARK
APPLICANT: DANIEL L. EATON
APPLICANT: AUSTIN L. GIBNEY
APPLICANT: BREND WRANIK
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF
FILE REFERENCE: P1996R1-US
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US/10/371,341
PRIOR FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapien
US-10-371-341-2

Query Match 100.0%; Score 1552; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTLPAMLTGKGLFWVFPLIPLYDINNIHKGSCDVOLYTKRQSEHSILAGDPFLBCFV 60
DB 1 MKTLPAMLTGKGLFWVFPLIPLYDINNIHKGSCDVOLYTKRQSEHSILAGDPFLBCFV 60
QY 61 KYCANRHHVWCKLNGTTCYCLBDRQTSWKEKNISFFIHFBEVTLFNDNSYRCSANFQ 120
DB 61 KYCANRHHVWCKLNGTTCYCLBDRQTSWKEKNISFFIHFBEVTLFNDNSYRCSANFQ 120
QY 121 SNLBSHSTLYVTDVASASERPSKDMARPMILYSLPLGGLPLITTCFCFLCCLRR 180
DB 121 SNLBSHSTLYVTDVASASERPSKDMARPMILYSLPLGGLPLITTCFCFLCCLRR 180
QY 181 HOGKONELSTAGREINTLVDAHLKSEOTEASTRONSQVLLSEGTIYNDPDLCPRMQEGS 240
DB 181 HOGKONELSTAGREINTLVDAHLKSEOTEASTRONSQVLLSEGTIYNDPDLCPRMQEGS 240
QY 241 EYVSNPFLSKNKRGIVYASLNHSYTGNSRLANVKEAPTEVASICRS 289
DB 241 EYVSNPFLSKNKRGIVYASLNHSYTGNSRLANVKEAPTEVASICRS 289
RESULT 2
US-10-600-997-6

RESULT 2

US-10-371-341-2
 / Sequence 2, Application US/10371341
 / Publication No. US20040091864A1
 / GENERAL INFORMATION:
 / APPLICANT: HILARY CLARK
 / APPLICANT: DANIEL L. EATON
 / APPLICANT: AUSTIN L. GURNEY
 / APPLICANT: BERNI WRANIK
 / TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF
 / TITLE OF INVENTION: IMMUNE RELATED DISEASES
 / FILE REFERENCE: P1996R1-US
 / CURRENT APPLICATION NUMBER: US/10/371,341
 / CURRENT FILING DATE: 2003-02-19
 / PRIOR APPLICATION NUMBER: US 60/421,236
 / PRIOR FILING DATE: 2002-10-25
 / NUMBER OF SEQ ID NOS: 2
 / SEQ ID NO 2
 / LENGTH: 289
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-371-341-2

Query Match 97.4%; Score 1516; DB 4; Length 289;
 Best Local Similarity 97.9%; Pred. No. 1.5e-145;
 Matches 283; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 DB 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 QY KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 DB KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 QY 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 DB 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 QY 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 DB 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 QY 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289
 DB 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289

RESULT 3

US-10-600-997-6
 / Sequence 6, Application US/10600997
 / Publication No. US20040175380A1
 / GENERAL INFORMATION:
 / APPLICANT: Allison, James
 / APPLICANT: Murphy, Kenneth
 / APPLICANT: Matanabe, Norihiko
 / APPLICANT: Murphy, Theresa
 / APPLICANT: Yang, Jiaofei
 / APPLICANT: Yang, Xiangxing
 / TITLE OF INVENTION: Compositions and Methods for Modulating Lymphocyte Activity
 / FILE REFERENCE: A-71608/TAL/DHR
 / CURRENT APPLICATION NUMBER: US/10/600,997
 / CURRENT FILING DATE: 2003-06-20
 / PRIOR APPLICATION NUMBER: US 60/390,653
 / PRIOR FILING DATE: 2002-06-20
 / PRIOR APPLICATION NUMBER: US 60/438,593
 / PRIOR FILING DATE: 2003-01-06
 / NUMBER OF SEQ ID NOS: 56
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 6
 / LENGTH: 289

TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-600-997-6

Query Match 97.4%; Score 1516; DB 4; Length 289;
 Best Local Similarity 97.9%; Pred. No. 1.5e-145;
 Matches 283; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 DB 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 QY KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 DB KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 QY 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 DB 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 QY 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 DB 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 QY 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289
 DB 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289

RESULT 4

US-10-831-622-21
 / Sequence 21, Application US/10831622
 / Publication No. US20040248257A1
 / GENERAL INFORMATION:
 / APPLICANT: Kaye, Jonathan
 / APPLICANT: Wilkinson, Beverley
 / TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
 / FILE REFERENCE: TSRI 810.1
 / CURRENT APPLICATION NUMBER: US/10/831,622
 / CURRENT FILING DATE: 2004-04-23
 / PRIOR APPLICATION NUMBER: US 60/467,206
 / PRIOR FILING DATE: 2003-04-30
 / NUMBER OF SEQ ID NOS: 113
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 21
 / LENGTH: 289
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-831-622-21

Query Match 97.4%; Score 1516; DB 5; Length 289;
 Best Local Similarity 97.9%; Pred. No. 1.5e-145;
 Matches 283; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 DB 1 MRTLPMAGTGLFWFPLIPYLDIWNHKGSCDVOLYIKQSHSIIAGDPFELBCPV 60
 QY KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 DB KVCANRPHVTWCKLNGTTCVKLEDRQTSWKEBKNIISFPIIHPFVLPNDGSTRCSANPQ 120
 QY 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 DB 121 SNLISHSTLLVYTDVKSASRSPKDEVASRPMILYSLLPLGGLPLITTCFLPCLLR 180
 QY 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 DB 181 HOGKONELSDTAGREINLVDAHLKSBQTASTRONSQVLLSBAIYDNDPDLCFRMOEGS 240
 QY 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289
 DB 241 EVCANPCLEBNKPGIYVASLNSHVSIGLNSRLARNVKAAPTETASICVRS 289